

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/551, 655A  
Source: IFWP  
Date Processed by STIC: 10/12/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/551,655A

TIME: 09:38:14

Input Set : A:\80621031.APP

Output Set: N:\CRF4\10122006\J551655A.raw

3 <110> APPLICANT: AYABE, SHIN-ICHI  
 4 AKASHI, TOMOYOSHI  
 5 AOKI, TOSHIO  
 7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE  
 8 DEHYDRATASE AND APPLICATION OF THE SAME  
 10 <130> FILE REFERENCE: 8062-1031  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/551,655A  
 13 <141> CURRENT FILING DATE: 2005-09-28  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP04/04214  
 16 <151> PRIOR FILING DATE: 2004-03-25  
 18 <150> PRIOR APPLICATION NUMBER: JP 2003-092337  
 19 <151> PRIOR FILING DATE: 2003-03-28  
 21 <160> NUMBER OF SEQ ID NOS: 10  
 23 <170> SOFTWARE: PatentIn Ver. 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 328  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Glycyrrhiza echinata  
 30 <400> SEQUENCE: 1  
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 32 1 5 10 15  
 34 Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp Gly Thr Val Glu Arg Phe  
 35 20 25 30  
 37 Leu Gly Ser Ser Phe Val Pro Pro Ser Pro Glu Asp Pro Glu Thr Gly  
 38 35 40 45  
 40 Val Ser Thr Lys Asp Ile Val Ile Ser Glu Asn Pro Thr Ile Ser Ala  
 41 50 55 60  
 43 Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr Thr Glu Lys Leu Pro Ile  
 44 65 70 75 80  
 46 Leu Val Tyr Tyr His Gly Gly Ala Phe Cys Leu Glu Ser Ala Phe Ser  
 47 85 90 95  
 49 Phe Leu His Gln Arg Tyr Leu Asn Ile Val Ala Ser Lys Ala Asn Val  
 50 100 105 110  
 52 Leu Val Val Ser Ile Glu Tyr Arg Leu Ala Pro Glu His Pro Leu Pro  
 53 115 120 125  
 55 Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu Lys Trp Val Thr Ser His  
 56 130 135 140  
 58 Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala Asp Pro Trp Leu Ile Lys  
 59 145 150 155 160  
 61 His Gly Asp Phe Asn Arg Phe Tyr Ile Gly Gly Asp Thr Ser Gly Ala  
 62 165 170 175  
 64 Asn Ile Ala His Asn Ala Ala Leu Arg Val Gly Ala Glu Ala Leu Pro  
 65 180 185 190

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67 Gly Gly Leu Arg Ile Ala Gly Val Leu Ser Ala Phe Pro Leu Phe Trp
68      195      200      205
70 Gly Ser Lys Pro Val Leu Ser Glu Pro Val Glu Gly His Glu Lys Ser
71      210      215      220
73 Ser Pro Met Gln Val Trp Asn Phe Val Tyr Pro Asp Ala Pro Gly Gly
74 225      230      235      240
76 Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala Pro Gly Ala Pro Asn Leu
77      245      250      255
79 Ala Thr Leu Gly Cys Pro Lys Met Leu Val Phe Val Ala Gly Lys Asp
80      260      265      270
82 Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr Glu Ala Val Lys Glu Ser
83      275      280      285
85 Gly Trp Lys Gly Asp Val Glu Leu Ala Gln Tyr Glu Gly Glu Glu His
86      290      295      300
88 Cys Phe Gln Ile Tyr His Pro Glu Thr Glu Asn Ser Lys Asp Leu Ile
89 305      310      315      320
91 Gly Arg Ile Ala Ser Phe Leu Val
92      325
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96 <211> LENGTH: 1178
97 <212> TYPE: DNA
98 <213> ORGANISM: Glycyrrhiza echinata
100 <220> FEATURE:
101 <221> NAME/KEY: CDS
102 <222> LOCATION: (23)..(1006)
104 <400> SEQUENCE: 2
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107      1      5      10
109 aaa gag ata gac agg gag ctt cct cct ctt ctc cgg gtc tac aaa gat 100
110 Lys Glu Ile Asp Arg Glu Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp
111      15      20      25
113 gga acc gtg gag cga ttc cta ggc tca tcg ttt gta cca cct tcc cct 148
114 Gly Thr Val Glu Arg Phe Leu Gly Ser Ser Phe Val Pro Pro Ser Pro
115      30      35      40
117 gaa gac ccc gaa aca ggg gtt tcc acg aaa gac ata gta atc tca gaa 196
118 Glu Asp Pro Glu Thr Gly Val Ser Thr Lys Asp Ile Val Ile Ser Glu
119      45      50      55
121 aac ccc acc atc tct gct cgc gtt tac ctt cca aaa ctg aac aac acc 244
122 Asn Pro Thr Ile Ser Ala Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr
123      60      65      70
125 acc gag aag ctc cca atc ttg gtc tac tac cac ggc ggc gcg ttc tgc 292
126 Thr Glu Lys Leu Pro Ile Leu Val Tyr Tyr His Gly Gly Ala Phe Cys
127 75      80      85      90
129 ctc gaa tct gct ttc tcc ttc ctc cac caa cgc tac ctc aac atc gtt 340
130 Leu Glu Ser Ala Phe Ser Phe Leu His Gln Arg Tyr Leu Asn Ile Val
131      95      100      105
133 gct tcc aag gca aat gtt cta gta gtt tcc atc gag tac agg ctc gcc 388
134 Ala Ser Lys Ala Asn Val Leu Val Val Ser Ile Glu Tyr Arg Leu Ala

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135          110          115          120
137 cca gaa cac cct ctt ccg gct gca tat gaa gat ggt tgg tat gct ctc 436
138 Pro Glu His Pro Leu Pro Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu
139          125          130          135
141 aaa tgg gtc act tct cat tcc aca aac aac aac aaa ccc acc aac gct 484
142 Lys Trp Val Thr Ser His Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala
143          140          145          150
145 gac cca tgg ttg atc aaa cac ggt gat ttc aac agg ttc tac atc ggg 532
146 Asp Pro Trp Leu Ile Lys His Gly Asp Phe Asn Arg Phe Tyr Ile Gly
147 155          160          165          170
149 ggt gac act tct ggt gca aac att gca cac aat gcg gct ctt cgt gtt 580
150 Gly Asp Thr Ser Gly Ala Asn Ile Ala His Asn Ala Ala Leu Arg Val
151          175          180          185
153 ggt gct gag gcc tta cct ggg ggg ctg aga ata gca ggg gta ctc tct 628
154 Gly Ala Glu Ala Leu Pro Gly Gly Leu Arg Ile Ala Gly Val Leu Ser
155          190          195          200
157 gct ttt cct ctg ttt tgg ggt tct aag cct gtt ttg tca gaa cct gtc 676
158 Ala Phe Pro Leu Phe Trp Gly Ser Lys Pro Val Leu Ser Glu Pro Val
159          205          210          215
161 gag ggg cat gag aag agc tca ccc atg caa gtt tgg aac ttt gtg tac 724
162 Glu Gly His Glu Lys Ser Ser Pro Met Gln Val Trp Asn Phe Val Tyr
163          220          225          230
165 cca gat gca cca ggt ggc ata gat aac cca cta atc aac cct ttg gca 772
166 Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala
167 235          240          245          250
169 cct ggg gct cct aac ttg gcc aca ctt ggg tgt cca aag atg ttg gtc 820
170 Pro Gly Ala Pro Asn Leu Ala Thr Leu Gly Cys Pro Lys Met Leu Val
171          255          260          265
173 ttt gtt gcg ggg aag gat gat ctt aga gac aga ggg att tgg tac tat 868
174 Phe Val Ala Gly Lys Asp Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr
175          270          275          280
177 gag gct gtg aag gaa agt ggg tgg aaa ggg gat gtg gaa ctt gct cag 916
178 Glu Ala Val Lys Glu Ser Gly Trp Lys Gly Asp Val Glu Leu Ala Gln
179          285          290          295
181 tat gaa ggg gag gaa cat tgc ttc cag atc tac cat cct gaa act gag 964
182 Tyr Glu Gly Glu Glu His Cys Phe Gln Ile Tyr His Pro Glu Thr Glu
183          300          305          310
185 aat tct aaa gat ctc atc ggt cgc atc gct tcc ttc ctt gtt 1006
186 Asn Ser Lys Asp Leu Ile Gly Arg Ile Ala Ser Phe Leu Val
187 315          320          325
189 tgaacacaca gctagacttc ggggttcatta ttactagtat gtgattttgt ttgattaatg 1066
191 ttttgtcatc aattgatggg taataaattg gattagggtta ctagggttcc tgaatcatgc 1126
193 tcaatttttac ttttcctgta ctattacttg tttatgaaag aattaatggc at 1178
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 319
198 <212> TYPE: PRT
199 <213> ORGANISM: Glycine max
201 <400> SEQUENCE: 3
202 Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr

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203      1              5              10              15
205 Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala
206              20              25              30
208 Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
209              35              40              45
211 Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
212              50              55              60
214 His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala
215      65              70              75              80
217 Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn
218              85              90              95
220 Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg
221              100              105              110
223 Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr
224              115              120              125
226 Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn
227      130              135              140
229 Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val
230 145              150              155              160
232 Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg
233              165              170              175
235 Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu
236              180              185              190
238 Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala
239              195              200              205
241 Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala
242      210              215              220
244 Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys
245 225              230              235              240
247 Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu
248              245              250              255
250 Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr
251              260              265              270
253 His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe
254              275              280              285
256 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
257      290              295              300
259 His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val
260 305              310              315
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264 <211> LENGTH: 960
265 <212> TYPE: DNA
266 <213> ORGANISM: Glycine max
268 <220> FEATURE:
269 <221> NAME/KEY: CDS
270 <222> LOCATION: (1)..(957)
272 <400> SEQUENCE: 4
273 atg gcg aag gag ata gtg aaa gag ctt ctt cct cta att cga gtg tac      48
274 Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr

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## RAW SEQUENCE LISTING

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| 275 | 1   |     | 5   |     | 10  |     | 15  |     |     |     |     |     |     |     |     |     |  |  |     |
| 277 | aag | gat | ggc | agc | gtg | gag | cgt | ctt | cta | agc | tct | gaa | aac | gtg | gca | gcc |  |  | 96  |
| 278 | Lys | Asp | Gly | Ser | Val | Glu | Arg | Leu | Leu | Ser | Ser | Glu | Asn | Val | Ala | Ala |  |  |     |
| 279 |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |  |     |
| 281 | tcc | cct | gaa | gat | ccc | caa | act | gga | gtc | tca | tcc | aaa | gac | ata | gtc | atc |  |  | 144 |
| 282 | Ser | Pro | Glu | Asp | Pro | Gln | Thr | Gly | Val | Ser | Ser | Lys | Asp | Ile | Val | Ile |  |  |     |
| 283 |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |  |  |     |
| 285 | gca | gac | aac | ccc | tac | gtc | tcc | gct | cgc | att | ttc | ctt | ccc | aaa | tcc | cac |  |  | 192 |
| 286 | Ala | Asp | Asn | Pro | Tyr | Val | Ser | Ala | Arg | Ile | Phe | Leu | Pro | Lys | Ser | His |  |  |     |
| 287 |     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |  |  |     |
| 289 | cac | act | aac | aac | aaa | ctc | ccc | atc | ttc | ctc | tac | ttc | cac | ggg | ggc | gcc |  |  | 240 |
| 290 | His | Thr | Asn | Asn | Lys | Leu | Pro | Ile | Phe | Leu | Tyr | Phe | His | Gly | Gly | Ala |  |  |     |
| 291 | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |     |     |     |  |  |     |
| 293 | ttt | tgc | gtc | gaa | tcc | gcc | ttc | tcc | ttt | ttc | gtc | cac | cgc | tat | ctc | aac |  |  | 288 |
| 294 | Phe | Cys | Val | Glu | Ser | Ala | Phe | Ser | Phe | Phe | Val | His | Arg | Tyr | Leu | Asn |  |  |     |
| 295 |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |     |  |  |     |
| 297 | atc | ttg | gcc | tca | gaa | gcc | aac | ata | ata | gcc | atc | tcc | gtc | gac | ttc | aga |  |  | 336 |
| 298 | Ile | Leu | Ala | Ser | Glu | Ala | Asn | Ile | Ile | Ala | Ile | Ser | Val | Asp | Phe | Arg |  |  |     |
| 299 |     | 100 |     |     |     | 105 |     |     | 110 |     |     |     |     |     |     |     |  |  |     |
| 301 | ctc | ctc | cca | cac | cac | cct | atc | cct | gct | gcc | tac | gaa | gac | ggg | tgg | acc |  |  | 384 |
| 302 | Leu | Leu | Pro | His | His | Pro | Ile | Pro | Ala | Ala | Tyr | Glu | Asp | Gly | Trp | Thr |  |  |     |
| 303 |     | 115 |     |     |     | 120 |     |     | 125 |     |     |     |     |     |     |     |  |  |     |
| 305 | acc | ctc | aaa | tgg | att | gct | tcc | cac | gcc | aac | aac | acc | aac | acc | acc | aac |  |  | 432 |
| 306 | Thr | Leu | Lys | Trp | Ile | Ala | Ser | His | Ala | Asn | Asn | Thr | Asn | Thr | Thr | Asn |  |  |     |
| 307 |     | 130 |     |     |     | 135 |     |     | 140 |     |     |     |     |     |     |     |  |  |     |
| 309 | ccg | gag | cca | tgg | cta | ctc | aac | cac | gcc | gac | ttc | acc | aaa | gtc | tac | gta |  |  | 480 |
| 310 | Pro | Glu | Pro | Trp | Leu | Leu | Asn | His | Ala | Asp | Phe | Thr | Lys | Val | Tyr | Val |  |  |     |
| 311 | 145 |     |     | 150 |     |     | 155 |     |     |     | 160 |     |     |     |     |     |  |  |     |
| 313 | gga | ggg | gaa | acc | agc | ggg | gct | aac | atc | gca | cac | aac | ctg | ctt | ttg | cgt |  |  | 528 |
| 314 | Gly | Gly | Glu | Thr | Ser | Gly | Ala | Asn | Ile | Ala | His | Asn | Leu | Leu | Leu | Arg |  |  |     |
| 315 |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |     |  |  |     |
| 317 | gca | ggg | aac | gaa | tcc | ctc | ccc | ggg | gat | ctg | aaa | ata | ttg | ggg | gga | tta |  |  | 576 |
| 318 | Ala | Gly | Asn | Glu | Ser | Leu | Pro | Gly | Asp | Leu | Lys | Ile | Leu | Gly | Gly | Leu |  |  |     |
| 319 |     | 180 |     |     |     | 185 |     |     | 190 |     |     |     |     |     |     |     |  |  |     |
| 321 | cta | tgc | tgc | ccc | ttc | ttc | tgg | ggc | tcg | aag | cca | att | ggg | tcg | gag | gct |  |  | 624 |
| 322 | Leu | Cys | Cys | Pro | Phe | Phe | Trp | Gly | Ser | Lys | Pro | Ile | Gly | Ser | Glu | Ala |  |  |     |
| 323 |     | 195 |     |     |     | 200 |     |     | 205 |     |     |     |     |     |     |     |  |  |     |
| 325 | gtt | gag | ggg | cac | gag | cag | agt | ttg | gcc | atg | aag | gtc | tgg | aac | ttt | gcc |  |  | 672 |
| 326 | Val | Glu | Gly | His | Glu | Gln | Ser | Leu | Ala | Met | Lys | Val | Trp | Asn | Phe | Ala |  |  |     |
| 327 |     | 210 |     |     |     | 215 |     |     | 220 |     |     |     |     |     |     |     |  |  |     |
| 329 | tgc | cct | gat | gcc | ccc | ggg | gga | atc | gat | aac | ccc | tgg | atc | aac | ccc | tgt |  |  | 720 |
| 330 | Cys | Pro | Asp | Ala | Pro | Gly | Gly | Ile | Asp | Asn | Pro | Trp | Ile | Asn | Pro | Cys |  |  |     |
| 331 | 225 |     |     | 230 |     |     | 235 |     |     |     | 240 |     |     |     |     |     |  |  |     |
| 333 | gtt | cct | ggg | gca | ccc | tct | ttg | gcc | act | ctt | gcc | tgc | tct | aag | ttg | ctc |  |  | 768 |
| 334 | Val | Pro | Gly | Ala | Pro | Ser | Leu | Ala | Thr | Leu | Ala | Cys | Ser | Lys | Leu | Leu |  |  |     |
| 335 |     |     | 245 |     |     |     | 250 |     |     |     | 255 |     |     |     |     |     |  |  |     |
| 337 | gtt | act | atc | act | ggc | aaa | gac | gag | ttc | aga | gac | aga | gat | att | ctc | tac |  |  | 816 |
| 338 | Val | Thr | Ile | Thr | Gly | Lys | Asp | Glu | Phe | Arg | Asp | Arg | Asp | Ile | Leu | Tyr |  |  |     |
| 339 |     |     | 260 |     |     |     | 265 |     |     |     | 270 |     |     |     |     |     |  |  |     |

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/551,655A

DATE: 10/12/2006

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Input Set : A:\80621031.APP

Output Set: N:\CRF4\10122006\J551655A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number